

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 02:08:12 ; Search time 5587 Seconds
(without alignments)
11344.088 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 1308
Sequence: 1 atgcaggacaggccaggag.....aaatccactaaatcctag 1308

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1308	100.0	1743	6	AX191430	Sequence
2	1308	100.0	1743	6	AX454638	Sequence
3	1308	100.0	1743	6	AX491116	Sequence
4	1308	100.0	1743	6	AX697167	Sequence
5	1308	100.0	1743	9	AX358700	Homo sapi
6	1308	100.0	1766	6	AX675079	Sequence
7	1298.4	99.3	1313	6	AR541803	Sequence
8	1298.4	99.3	1710	6	AR560132	Sequence
9	1295.2	99.0	1787	9	AY220118	Homo sapi
10	1270.4	97.1	1581	6	AX392981	Sequence
11	1270.4	97.1	1759	6	AX35862	Sequence
12	1263.4	96.6	1329	6	AX135904	Sequence
13	1262.4	96.5	1250	6	AX392967	Sequence
14	1244.4	95.1	1254	6	CQ735615	Sequence
15	1182.8	90.4	1194	6	AX135908	Sequence
16	1097	83.9	1346	9	AY185496	Homo sapi
17	1073.4	82.1	1548	9	AY220120	Homo sapi
18	872	66.7	1156	9	AY185497	Homo sapi
19	869.8	66.5	1489	9	AY220121	Homo sapi

20	733.6	56.1	1451	9	AY220119	Homo sapi
21	647.2	49.5	147505	9	CNS01DPA	Human chr
22	647.2	49.5	181004	9	CNS01DPA	Human chr
23	537.8	41.1	1365	9	BC020747	Homo sapi
24	537.8	41.1	1872	6	AX409610	Sequence
25	537.8	41.1	1872	9	HUMTBG	Human thyro
26	536.6	41.0	1280	4	AP204928	Bos tauru
27	534.6	40.9	1432	6	AR531797	Sequence
28	525.4	40.2	1395	4	ONTEG	Sequence
29	519.6	39.7	1785	6	CQ716276	Sequence
30	518.4	39.6	1284	4	AP204929	Sus scro
31	488.6	37.4	1714	6	AX401745	Sequence
32	488.6	37.4	1714	10	RATTBGA	Rat thyroxi
33	476.8	36.5	1388	10	AX575783	Sequence
34	373.2	28.5	1428	6	AX642662	Sequence
35	373.2	28.5	1428	9	HUMAACTA	Human alpha
36	373.2	28.5	1466	6	BD176851	A method
37	373.2	28.5	1466	6	AX770543	Sequence
38	373.2	28.5	1466	9	AF089747	Homo sapi
39	373.2	28.5	1522	6	CQ802318	Sequence
40	373.2	28.5	1522	6	CQ814554	Sequence
41	373.2	28.5	1522	6	AX642661	Sequence
42	373.2	28.5	1528	6	CQ720070	Sequence
43	373.2	28.5	1592	9	BC010530	Homo sapi
44	373.2	28.5	1603	9	BC003559	Homo sapi
45	373.2	28.5	2480	6	AX747885	Sequence

ALIGNMENTS

RESULT 1	AX191430	Sequence 5 from Patent WO0149715.	1743 bp	DNA	linear	PAT 15-AUG-2001
LOCUS	AX191430					
DEFINITION	AX191430					
ACCESSION	AX191430					
VERSION	AX191430.1	GI:15209638				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1					
AUTHORS	Ashkenazi,A.J., Goddard,A., Gurney,A.L., Napier,M.A., Watanabe,C.K. and Wood,W.I.					
TITLE	Methods and compositions for inhibiting neoplastic cell growth					
JOURNAL	Patent: WO 0149715-A 5 12-JUL-2001;					
	Genentech, Inc. (US)					
FEATURES	Location/Qualifiers					
source	1..1743					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					

ORIGIN

Query Match	100.0%	Score 1308;	DB 6;	Length 1743;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1308;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCAAGCAGGGCAGGAGGAGGACCTGCAAGACATATTTGTTCCAAATGGCA	60	
DB	6	ATGCAAGCAGGGCAGGAGGAGGACCTGCAAGACATATTTGTTCCAAATGGCA	65	
QY	61	TCTTACCTTTATGGAGTACTCTTTGCTGTGGCTCTGTGCTCCAATCTACTGTGTGTC	120	
DB	66	TCTTACCTTTATGGAGTACTCTTTGCTGTGGCTCTGTGCTCCAATCTACTGTGTGTC	125	
QY	121	CGGGCAATGCCCCCAGTGTCATACCCCGCCCTTCTCCACAAGAGCACCCTGCCTCA	180	
DB	126	CGGGCAATGCCCCCAGTGTCATACCCCGCCCTTCTCCACAAGAGCACCCTGCCTCA	185	
QY	181	CAGGTGTTATTCCTCAACCGACTTTGCTCCGCTTCCGCTTACCGAGGCTGTTTGGAG	240	

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 02:01:07 ; Search time 723 Seconds
(without alignments)
10709.574 Million cell updates/sec

Title: US-09-993-180-1_copy_68_1375
Perfect score: 1308
Sequence: 1 atgcaaggacaggcaggag.....aaatcccaataatcctag 1308

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308	100.0	1743	3	AAA37089
2	1308	100.0	1743	4	AAFS4367
3	1308	100.0	1743	4	AS46150
4	1308	100.0	1743	6	ABL88183
5	1308	100.0	1743	6	ABK11752
6	1308	100.0	1743	6	ABL95672
7	1308	100.0	1743	8	ACA89600
8	1308	100.0	1743	8	ACA73610
9	1308	100.0	1743	8	ACA05925
10	1308	100.0	1743	8	ACA66759
11	1308	100.0	1743	8	ACF20334
12	1308	100.0	1743	8	ACF19720
13	1308	100.0	1743	8	ACD22008
14	1308	100.0	1743	8	ACF13173
15	1308	100.0	1743	8	ACD25276
16	1308	100.0	1743	8	ACF00325
17	1308	100.0	1743	8	ACA72382
18	1308	100.0	1743	8	ACD04906
19	1308	100.0	1743	8	ACD18367
20	1308	100.0	1743	8	ACD08374

21	1308	100.0	1743	8	ACA88808	Novel hum
22	1308	100.0	1743	8	ACA70250	Human sec
23	1308	100.0	1743	8	ACD12472	Novel hum
24	1308	100.0	1743	8	ACC74387	Human sec
25	1308	100.0	1743	8	ACD16015	Human sec
26	1308	100.0	1743	8	ACD25583	Novel hum
27	1308	100.0	1743	8	ACD18060	Human sec
28	1308	100.0	1743	8	ACC88347	Human sec
29	1308	100.0	1743	8	ACD21701	Human sec
30	1308	100.0	1743	8	ABX98378	Human CDN
31	1308	100.0	1743	8	ACD14129	Human PRO
32	1308	100.0	1743	8	ACD09909	Human sec
33	1308	100.0	1743	8	ACC88654	Human sec
34	1308	100.0	1743	8	ACD21394	Human sec
35	1308	100.0	1743	8	ABX75766	Human CDN
36	1308	100.0	1743	8	ABX97969	Human PRO
37	1308	100.0	1743	8	ACA97445	Novel hum
38	1308	100.0	1743	8	ACA57908	Human PRO
39	1308	100.0	1743	8	ACD14436	Human PRO
40	1308	100.0	1743	8	ACC91219	Human sec
41	1308	100.0	1743	8	ACC88961	Human sec
42	1308	100.0	1743	8	ACD07158	Human PRO
43	1308	100.0	1743	8	ACA57609	Human PRO
44	1308	100.0	1743	8	ACC81664	Human sec
45	1308	100.0	1743	8	ACC89268	Human sec

ALIGNMENTS

RESULT 1
AAA37089
ID AAA37089 standard; cDNA; 1743 BP.
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AC AAA37089;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1337 (UNQ692) cDNA sequence SEQ ID NO:235.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX Homo sapiens.
OS
PN WC200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99MO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 03-SEP-1998; 98US-0098936P.
PR 03-SEP-1998; 98US-0098959P.
PR 03-SEP-1998; 98US-0098960P.
PR 03-SEP-1998; 98US-0098962P.
PR 03-SEP-1998; 98US-0098964P.
PR 03-SEP-1998; 98US-0098974P.
PR 10-SEP-1998; 98US-0098754P.
PR 10-SEP-1998; 98US-0098763P.
PR 10-SEP-1998; 98US-0098979P.
PR 10-SEP-1998; 98US-0098980P.
PR 10-SEP-1998; 98US-0098981P.
PR 10-SEP-1998; 98US-0098981P.
PR 10-SEP-1998; 98US-0098981P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.

Result No.	Query			ID	Description
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1	1244.4	95.1	1254	9	AY401148 Homo sapi
2	1140.6	87.2	1228	9	AY401149 Pan trogl
3	742.6	56.8	906	4	BG758811 602713172
4	735	56.2	813	4	BG756763 602710234
5	730.4	55.8	1073	4	BM455692 AGENCOURT
6	725	55.4	1257	9	AY401150 Mus muscu
7	725	55.4	1694	3	AK009343 Mus muscu
8	708.2	54.1	816	4	BG684028 BG5635635
9	695.6	53.2	946	2	BF794222 602255418
10	684	52.3	1097	4	BF975146 602244622
11	617.6	47.2	784	4	BG035642 602325711
12	612.2	46.8	702	4	BI871087 6032394260
13	612.2	46.8	771	4	BG398393 602439864
14	533.4	40.8	576	2	BF128752 601811131
15	440	33.6	447	2	AW408367 UI-HF-BKO
16	373.2	28.5	1487	3	CR609815 full-length
17	373.2	28.5	1499	3	CR619614 full-length
18	373.2	28.5	1501	3	CR590750 full-length
19	373.2	28.5	1503	3	CR612671 full-length
20	373.2	28.5	1503	3	CR623490 full-length
21	373.2	28.5	1504	3	CR620654 full-length
22	373.2	28.5	1505	3	CR595639 full-length
23	373.2	28.5	1506	3	CR592388 full-length
24	373.2	28.5	1512	3	CR605766 full-length

Query Match	95.1%	Score 1244.4	DB 9	Length 1254
Best Local Similarity	99.5%	Pred. NO. 0		
Matches 1248	Conservative	0	Mismatches 6	Indels 0
Gaps	0			

QY	55	ATGGCATCTTACCTTTATGGAGTACTCTTTGTGTTGGCTCTGTGCTCCAACTACTGT	114
DB	1	ATGGCATCTTACCTTTATGGAGTACTCTTTGTGTTGGCTCTGTGCTCCAACTACTGT	60

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 03:12:08 ; Search time 258 Seconds
(without alignments)
8295.542 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375
Perfect score: 1308
Sequence: 1 atgcaaggacaggaggag.....aaatcccaactaaatccttag 1308

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCRTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1298.4	99.3	1313	4	US-09-774-528-51
2	1298.4	99.3	1710	4	US-09-912-628-2
3	539.4	41.2	1878	4	US-09-949-016-5670
4	534.6	40.9	1432	4	US-09-919-039-389
5	373.2	28.5	5193	4	US-09-976-594-1126
6	371.6	28.4	1580	4	US-09-976-594-18
7	371.6	28.4	1580	4	US-09-919-039-18
8	356.2	27.2	1527	4	US-09-244-111-7
9	326.6	25.0	1245	4	US-09-949-016-2272
10	306	23.4	1185	3	US-09-023-339-2
11	306	23.4	5932	3	US-09-299-141-4
12	306	23.4	6142	3	US-09-299-141-8
13	306	23.4	6565	3	US-09-299-141-1
14	306	23.4	6714	3	US-09-299-141-6
15	306	23.4	6924	3	US-09-299-141-9
16	306	23.4	6924	3	US-09-299-141-10
17	306	23.4	6924	3	US-09-299-141-11
18	306	23.4	6981	3	US-09-299-141-7
19	306	23.4	7054	3	US-09-299-141-3
20	306	23.4	7405	3	US-09-299-141-2
21	304.4	23.3	1417	4	US-10-000-489-91
22	289.6	22.1	8190	4	US-09-949-016-17412
23	288	22.0	1356	1	US-08-002-202-12
24	288	22.0	1356	1	US-08-002-202-18
25	288	22.0	1356	3	US-08-481-534-12
26	288	22.0	1356	3	US-08-481-534-18
27	286.4	21.9	1356	1	US-08-002-202-16

28	286.4	21.9	1356	3	US-08-481-534-16	Sequence 16, Appl
29	285.8	21.9	1423	1	US-07-829-954-1	Sequence 1, Appl
30	285.8	21.9	1423	1	US-07-994-423-1	Sequence 1, Appl
31	285.8	21.9	1423	1	US-08-421-891-1	Sequence 1, Appl
32	284.2	21.7	1476	4	US-09-949-016-1726	Sequence 1726, Ap
33	271.2	20.7	1266	4	US-09-949-016-2294	Sequence 2294, Ap
34	260	19.9	1194	4	US-10-000-489-49	Sequence 49, Appl
35	254.4	19.4	1263	4	US-09-949-016-834	Sequence 834, App
36	253.8	19.4	1185	3	US-09-023-339-3	Sequence 3, Appl
37	253.8	19.4	1260	3	US-09-023-173-5	Sequence 5, Appl
38	253.8	19.4	1308	3	US-09-023-173-10	Sequence 10, Appl
39	253.8	19.4	1308	3	US-09-023-339-6	Sequence 6, Appl
40	233.4	17.8	1245	4	US-09-755-665-13	Sequence 13, Appl
41	233.4	17.8	1445	4	US-09-461-325-13	Sequence 13, Appl
42	233.4	17.8	1445	4	US-10-012-542-13	Sequence 13, Appl
43	233.4	17.8	1445	4	US-10-115-123-13	Sequence 13, Appl
44	197.6	15.1	1339	1	US-07-859-480-1	Sequence 1, Appl
45	189.2	14.5	8896	4	US-09-949-016-14014	Sequence 14014, A

ALIGNMENTS

RESULT 1
US-09-774-528-51
; Sequence 51, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/774,528
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: PC_FL_genes Version 2.0
; SEQ ID NO 51
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1313)
US-09-774-528-51

Query Match 99.3%; Score 1298.4; DB 4; Length 1313;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATCAAGGACAGGGCAGGAGAACTGCAAGACATATTTTGTCCAAATGGCA 60
DB 6 ATCAAGGACAGGGCAGGAGAACTGCAAGACATATTTTGTCCAAATGGCA 65
QY 61 TCTTACCTTATGAGTACTCTTTGTGTGGCTCTGCTCCAATCTACTGTGTCC 120
DB 66 TCTTACCTTATGAGTACTCTTTGTGTGGCTCTGCTCCAATCTACTGTGTCC 125
QY 121 CGGGCCAATGCCCAAGTGCATACCCCGCCCTTCTCCCAAGAGACCCCTGCTCA 180
DB 126 CGGGCCAATGCCCAAGTGCATACCCCGCCCTTCTCCCAAGAGACCCCTGCTCA 185

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 04:52:59 ; Search time 912 Seconds
(without alignments)
9989.049 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 1308

Sequence: 1 atgcaagacagggcaggag.....aaaatccactaaatcttag 1308

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/PCTUS_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1308	100.0	1743	10	US-09-946-374-235
2	1308	100.0	1743	14	US-10-006-856A-235
3	1308	100.0	1743	14	US-10-184-644-451
4	1308	100.0	1743	14	US-10-006-818A-235
5	1308	100.0	1743	14	US-10-006-485A-235
6	1308	100.0	1743	14	US-10-013-907A-235
7	1308	100.0	1743	14	US-10-015-499A-235

8	1308	100.0	1743	14	US-10-184-634-451	Sequence 451, App
9	1308	100.0	1743	14	US-10-015-393A-235	Sequence 235, App
10	1308	100.0	1743	14	US-10-015-869A-235	Sequence 235, App
11	1308	100.0	1743	14	US-10-012-121A-235	Sequence 235, App
12	1308	100.0	1743	14	US-10-006-116A-235	Sequence 235, App
13	1308	100.0	1743	14	US-10-006-117A-235	Sequence 235, App
14	1308	100.0	1743	14	US-10-017-527A-235	Sequence 235, App
15	1308	100.0	1743	14	US-10-013-913A-235	Sequence 235, App
16	1308	100.0	1743	14	US-10-007-194A-235	Sequence 235, App
17	1308	100.0	1743	14	US-10-013-430A-235	Sequence 235, App
18	1308	100.0	1743	14	US-10-011-671A-235	Sequence 235, App
19	1308	100.0	1743	14	US-10-012-755A-235	Sequence 235, App
20	1308	100.0	1743	14	US-10-015-386A-235	Sequence 235, App
21	1308	100.0	1743	15	US-10-223-085-223	Sequence 223, App
22	1308	100.0	1743	15	US-10-223-084-223	Sequence 223, App
23	1308	100.0	1743	15	US-10-223-088-223	Sequence 223, App
24	1308	100.0	1743	15	US-10-223-090-223	Sequence 223, App
25	1308	100.0	1743	15	US-10-223-087-223	Sequence 223, App
26	1308	100.0	1743	15	US-10-011-692A-235	Sequence 235, App
27	1308	100.0	1743	15	US-10-006-768A-235	Sequence 235, App
28	1308	100.0	1743	15	US-10-017-610A-235	Sequence 235, App
29	1308	100.0	1743	15	US-10-006-063A-235	Sequence 235, App
30	1308	100.0	1743	15	US-10-020-063A-235	Sequence 235, App
31	1308	100.0	1743	15	US-10-223-083-223	Sequence 223, App
32	1308	100.0	1743	15	US-10-015-391A-235	Sequence 235, App
33	1308	100.0	1743	15	US-10-223-089-223	Sequence 223, App
34	1308	100.0	1743	15	US-10-017-407A-235	Sequence 223, App
35	1308	100.0	1743	15	US-10-011-833A-235	Sequence 235, App
36	1308	100.0	1743	15	US-10-006-041A-235	Sequence 235, App
37	1308	100.0	1743	15	US-10-015-822A-235	Sequence 235, App
38	1308	100.0	1743	15	US-10-015-387A-235	Sequence 235, App
39	1308	100.0	1743	15	US-10-006-130A-235	Sequence 235, App
40	1308	100.0	1743	16	US-10-006-172A-235	Sequence 235, App
41	1308	100.0	1743	16	US-10-017-253A-235	Sequence 235, App
42	1308	100.0	1743	16	US-10-015-392A-235	Sequence 235, App
43	1308	100.0	1743	16	US-10-017-306A-235	Sequence 235, App
44	1308	100.0	1743	16	US-10-017-867A-235	Sequence 235, App
45	1308	100.0	1743	16	US-10-012-064A-235	Sequence 235, App

ALIGNMENTS

RESULT 1
US-09-946-374-235
; Sequence 235, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC1
; CURRENT APPLICATION NUMBER: US/09/946,374

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 9, 2005, 06:00:34 ; Search time: 114.5 Seconds
(without alignments)
8336.377 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 2444

Sequence: 1 atgcaagagacaggcaggag.....aaaatccactaaatctctag 1308

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp
-Q=/cgn2 1/USPTO.epool p/US09993180/runat 07102005 180815 18615/app_query.fasta 1.1479
-DB=A Geneseq 16Dec04 -QWTF=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPTCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USMR=US09993180 -CGN 1 154 -runat 07102005 180815 18615 -NCPU=6 -ICPU=3
-NO MMAP -LARGESCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq 16Dec04:

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2225	91.0	435	5 AAE25298	Aae25298 Human LSI
2	2202	90.1	435	4 AAO14912	Aao14912 Human ser
3	2124	86.9	417	3 AAY99407	Aay99407 Human PRO
4	2124	86.9	417	4 AAB66156	Aab66156 Protein o
5	2124	86.9	417	4 AAU28249	Aau28249 Human PRO
6	2124	86.9	417	5 ABG70636	Abg70636 Human ser
7	2124	86.9	417	5 ABB84928	Abb84928 Human PRO
8	2124	86.9	417	5 AAU77792	Aau77792 Human PRO
9	2124	86.9	417	5 ABB95534	Abb95534 Human ang
10	2124	86.9	417	6 ABU58625	Abu58625 Human PRO

11	2124	86.9	417	6 ABU88173	Abu88173 Novel hum
12	2124	86.9	417	6 ABU84488	Abu84488 Human sec
13	2124	86.9	417	6 ABR66362	AbR66362 Human sec
14	2124	86.9	417	6 ABR65752	AbR65752 Human sec
15	2124	86.9	417	6 ABU99692	AbU99692 Human sec
16	2124	86.9	417	6 ABU82931	AbU82931 Human PRO
17	2124	86.9	417	6 ABU90052	AbU90052 Novel hum
18	2124	86.9	417	6 ABR68301	AbR68301 Human sec
19	2124	86.9	417	6 ABU96354	AbU96354 Novel hum
20	2124	86.9	417	6 ABU92785	AbU92785 Human sec
21	2124	86.9	417	6 ABO08862	AbO08862 Human sec
22	2124	86.9	417	6 ABO02914	AbO02914 Human sec
23	2124	86.9	417	6 ABR75068	AbR75068 Human sec
24	2124	86.9	417	6 ABR94830	AbR94830 Human sec
25	2124	86.9	417	6 ABU85803	AbU85803 Human PRO
26	2124	86.9	417	6 ABU98963	AbU98963 Novel hum
27	2124	86.9	417	6 ABU98178	AbU98178 Novel hum
28	2124	86.9	417	6 ABU91884	AbU91884 Novel hum
29	2124	86.9	417	6 ABU89577	AbU89577 Human PRO
30	2124	86.9	417	6 ABU86418	AbU86418 Human sec
31	2124	86.9	417	6 ABU67631	AbU67631 Human sec
32	2124	86.9	417	6 ABU80659	AbU80659 Human PRO
33	2124	86.9	417	6 ABR99577	AbR99577 Human sec
34	2124	86.9	417	6 ABR98967	AbR98967 Human sec
35	2124	86.9	417	6 ABO16490	AbO16490 Human sec
36	2124	86.9	417	6 ABR92390	AbR92390 Human sec
37	2124	86.9	417	6 ABO19031	AbO19031 Human sec
38	2124	86.9	417	6 ABR78452	AbR78452 Human sec
39	2124	86.9	417	6 ABU85188	AbU85188 Novel hum
40	2124	86.9	417	6 ABO00327	AbO00327 Novel hum
41	2124	86.9	417	6 ABO11659	AbO11659 Human sec
42	2124	86.9	417	6 ABO02304	AbO02304 Human sec
43	2124	86.9	417	6 ABU88878	AbU88878 Novel hum
44	2124	86.9	417	6 ABU83573	AbU83573 Human sec
45	2124	86.9	417	6 ABO06374	AbO06374 Novel hum

ALIGNMENTS

RESULT 1

AAE25298

ID AAE25298 standard; protein; 435 AA.

XX

AC AAE25298;

XX

DT 30-OCT-2002 (first entry)

XX

DB Human LSI-01 protein.

XX

KW Human; lymphocyte serine protease inhibitor; serpin-01; LSI-01; stroke;
KW potassium channel beta subunit; cardiovascular; inflammatory disease;
KW cancer; blood; immune; T-cell malignancy leukaemia; gastrointestinal;
KW metabolic; proliferative; emphysema; liver cirrhosis; arteriosclerosis;
KW immunological disorder; rheumatoid arthritis; psoriasis; gene therapy;
KW autoimmune infertility; vascular disease; microvascular disease; ulcer;
KW diarrhoea; embolism; thrombosis; neurological; Alzheimer's disease;
KW epilepsy; cytostatic; hepatotropic; thrombolytic; cerebroprotective;
KW immunosuppressive; nootropic; neuroprotective; anticonvulsant;
KW antiinfertility.

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Peptide 1..38

FT Protein /label= Signal-peptide

FT Protein 39..435

FT Binding-site /notes= "Human mature LSI-01 protein"

FT Binding-site 63..80

FT /note= "Heparin binding region; This region is specifically referred in claim 34 of the specification"

FT /note= "Heparin binding region; This region is specifically referred in claim 34 of the specification"

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 9, 2005, 14:18:29 ; Search time 34.5 seconds
(without alignments)
7295.741 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 2444

Sequence: 1 atgcaaggacaggaggag.....aaaatcccaataatccctag 1308

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09993180/runat_07102005_180816_18637/app_query.fasta_1.1479
-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993180 -CGN_1_38 @runat_07102005_180816_18637 -NCPUP=6 -ICPU=3
-NO_MMAL -LARGESQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	42.8	415	2 A47224	thyroxine-binding
2	1044.5	42.7	418	2 A39567	thyroxine-binding
3	1029.5	42.1	412	2 I46421	thyroxine-binding
4	889.5	36.4	427	2 A49518	kallistatin precursor
5	852.5	34.9	406	2 A39339	protein C inhibitor
6	850	34.8	433	1 ITHUC	alpha-1-antichymot
7	847	34.7	418	2 S23675	contrapsin-related
8	833	34.1	418	2 JH0494	alpha-1-antichymot
9	829.5	33.9	417	2 S19724	kallikrein-binding
10	829.5	33.9	418	1 S31507	serine proteinase
11	821	33.6	408	2 S11320	alpha-1-antitrypsin
12	814.5	33.3	405	2 A39088	alpha-1-antitrypsin
13	806.5	33.0	413	2 A54968	alpha-1-antitrypsin
14	801	32.8	413	2 S54981	alpha-1-antitrypsin

15	800	32.7	413	2 JX0267	alpha-1-antitrypsin
16	799	32.7	403	2 S08102	serine proteinase
17	798	32.7	418	2 JX0129	contrapsin precursor
18	795	32.5	411	1 ITRT	alpha-1-antitrypsin
19	793	32.4	410	2 A45457	alpha-1-antitrypsin
20	792	32.4	413	2 JX0154	alpha-1-antitrypsin
21	790.5	32.3	412	2 S31505	serine proteinase
22	788.5	32.3	406	2 JX0346	alpha-1-antitrypsin
23	788	32.2	410	2 C39088	contrapsin precursor
24	787	32.2	416	2 B29131	kallikrein-binding
25	779	31.9	383	2 A36117	corticosteroid-binding
26	779	31.9	416	1 ITHU	alpha-1-antitrypsin
27	778.5	31.9	405	2 A28321	corticosteroid-binding
28	777	31.8	430	2 A49190	corticosteroid-binding
29	774.5	31.7	413	2 I49474	alpha-1-antitrypsin
30	774.5	31.7	413	2 I56481	alpha-1-antitrypsin
31	771	31.5	409	1 ITHA	alpha-1-antitrypsin
32	770.5	31.5	413	2 I49470	alpha-1-antitrypsin
33	769	31.5	416	2 S21097	alpha-1-antitrypsin
34	768.5	31.4	413	2 I49452	alpha-1-antitrypsin
35	768	31.4	418	1 ITHU	alpha-1-antitrypsin
36	767	31.4	413	2 S60036	alpha-1-antitrypsin
37	765.5	31.3	413	2 I49472	alpha-1-antitrypsin
38	759.5	31.1	413	2 I49473	alpha-1-antitrypsin
39	757	31.0	406	2 I53281	corticosteroid-binding
40	756.5	31.0	402	2 I49471	alpha-1-antitrypsin
41	744	30.4	388	2 B39088	alpha-1-antitrypsin
42	705.5	28.9	410	2 I50494	serine proteinase
43	697	28.5	412	1 ITMSC	alpha-1-antitrypsin
44	692	28.3	369	2 JH0493	alpha-1-antichymot
45	668	27.3	420	2 A28882	alpha-1-antitrypsin

ALIGNMENTS

RESULT 1

A47224

thyroxine-binding globulin precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence revision 10-May-1996 #text_change 09-Jul-2004

C/Accession: A47224; S39801; A36479; A13535; S2190

R:Hayaishi, Y.; Mori, Y.; Janssen, O.E.; Sunthornthepvarakul, T.; Weiss, R.E.; Takeda, M.; Endocrinol. 7, 1049-1060, 1993

A>Title: Human thyroxine-binding globulin gene: complete sequence and transcriptional

A/Reference number: A47224; MUID:94049804; PMID:8232304

A/Accession: A47224

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-415 <RES>

A/Cross-references: UNIPROT:P05543; GB:L13470; NID:g405513; PIDN:AAA16067.1; PID:g4055

R/Akbari, M.T.; Kapadi, A.; Farmer, M.J.; Fitch, N.J.S.; McCann, K.P.; Kordestani, S.; Biochim. Biophys. Acta 1216, 446-454, 1993

A>Title: The structure of the human thyroxine binding globulin (TGB) gene.

A/Reference number: S39801; MUID:87017018; PMID:3094014

A/Accession: S39801

A/Status: preliminary; translation not shown

A/Molecule type: DNA

A/Residues: 1-415 <AKB>

A/Cross-references: EMBL:X64171; NID:g37141; PIDN:CAA45509.1; PID:g37142

R/Flink, I.L.; Bailey, T.J.; Gustafson, T.A.; Markham, B.E.; Morkin, E. Proc. Natl. Acad. Sci. U.S.A. 83, 7708-7712, 1986

A>Title: Complete amino acid sequence of human thyroxine-binding globulin deduced from

A/Reference number: A26479; MUID:87017018; PMID:3094014

A/Accession: A26479

A/Molecule type: mRNA

A/Residues: 1-196, 'T', 198-415 <FLI>

A/Cross-references: GB:M14091; NID:g338696; PIDN:AAA60616.1; PID:g338697

A/Note: the authors translated the codon GAG for residue 94 as Gly

R/Cheng, S.Y. Biochem. Biophys. Res. Commun. 79, 1212-1218, 1977

A/Reference number: A13535; MUID:78103214; PMID:414747

A/Accession: A13535

A/Molecule type: protein

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 9, 2005, 06:04:58 ; Search time 146.5 Seconds
(without alignments)
9144.022 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 2444

Sequence: 1 atgcaaggacagggcaggag.....aaatcccaataatctctag 1308

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MOLSL=frame+n2p.model
-Q=/cgn2.1/USPTO.spool.p/US09993180/runat_07102005_180816_18622/app_query.fasta_1.1479
-DB=UniProt_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOBL=0 -LOOEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45
-DICALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993180 @CCN_1.152 @runat_07102005_180816_18622 -NCPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

UniProt_03:*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2186	89.4	435	2 Q86WD7	Q86wd7 homo sapien
2	2124	86.9	417	2 Q6UMP9	Q6ump9 homo sapien
3	1867	76.4	370	2 Q85YP7	Q85yp7 homo sapien
4	1890	69.1	337	2 Q86WD5	Q86wd5 homo sapien
5	1640	67.1	335	2 Q86WD6	Q86wd6 homo sapien
6	1473	60.3	334	2 Q85YP6	Q85yp6 homo sapien
7	1429	58.5	286	2 Q86WD4	Q86wd4 homo sapien
8	1347	55.1	418	2 Q9D7D2	Q9d7d2 mus musculus
9	1057.5	43.3	412	1 THBG_PIG	Q9ctt35 mus scrofa
10	1047	42.8	415	1 THBG_HUMAN	P05543 homo sapien
11	1044.5	42.7	418	1 THBG_RAT	P35577 rattus norv
12	1042	42.6	415	1 THBG_PANTR	P61640 pan troglod
13	1040.5	42.6	411	1 THBG_BOVIN	Q9tt36 bos taurus
14	1029.5	42.1	412	1 THBG_SHEEP	P50450 ovis arie
15	1021.5	41.8	418	1 THBG_MOUSE	P61939 mus musculus
16	896.5	36.7	440	2 Q86UI7	Q86ui7 homo sapien

17	889.5	36.4	427	1 KAIN_HUMAN	P29622 homo sapien
18	889	36.4	445	2 Q86TR9	Q86tr9 homo sapien
19	872	35.7	423	1 AACT_HUMAN	P01011 homo sapien
20	864.5	35.4	415	2 Q9GMW6	Q9gma6 sus scrofa
21	861.5	35.2	407	2 Q9UNU9	Q9unu9 homo sapien
22	852.5	34.9	406	1 IPSP_HUMAN	P05154 homo sapien
23	847	34.7	418	2 Q03734	Q03734 mus musculus
24	843.5	34.5	405	1 IPSP_MOUSE	P70458 mus musculus
25	842	34.5	424	2 Q8CIE0	Q8cie0 mus musculus
26	841.5	34.4	405	2 Q8BU50	Q8bu50 m mus muscu
27	839	34.3	433	2 Q9YIB8	Q9yib8 xenopus lae
28	838.5	34.3	405	2 Q8BVN1	Q8bvn1 mus musculus
29	837.5	34.3	404	2 Q9N212	Q9n212 bos taurus
30	837.5	34.3	432	2 Q7SYX0	Q7syx0 xenopus lae
31	834	34.1	418	2 Q91WP6	Q91wp6 mus musculus
32	833	34.1	418	2 Q62258	Q62258 mus musculus
33	831.5	34.0	420	2 Q60552	Q60552 mesocricetu
34	830.5	34.0	413	1 ALMS_TAMSI	Q54758 tamias sibi
35	830.5	34.0	462	2 Q7TPA5	Q7tpa5 rattus norv
36	829.5	33.9	417	1 KBP_MOUSE	P29621 mus musculus
37	829.5	33.9	418	1 SI24_APOSY	Q60396 apodemus sy
38	828	33.9	418	1 CPI6_RAT	P09006 rattus norv
39	827	33.8	406	2 Q88292	Q88292 rattus norv
40	824	33.7	406	2 Q66HL5	Q66hl5 rattus norv
41	818.5	33.5	412	1 ALAT_CALCN	Q54763 callosciuru
42	817.5	33.4	413	2 Q76HN9	Q76hn9 tamias sibi
43	815.5	33.4	413	1 ALSI_TAMSI	Q54760 tamias sibi
44	814.5	33.3	405	1 ALAS_CAVPO	P22325 cavia porce
45	813	33.3	456	2 Q62663	Q62663 oryctolagus

ALIGNMENTS

RESULT 1

Q85WD7
ID Q86WD7
AC Q86WD7
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Germinal center B-cell expressed transcript 1 isoform A.
GN Name=GCET1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=22702315; PubMed=12819018;
RA Pan Z., Shen Y., Du C., Zhou G., Rosenwald A., Staudt L.M.,
RA Greiner T.C., McKeithan T.W., Chan W.C.;
RT "Two newly characterized germinal center B-cell-associated genes,
RT GCET1 and GCET2, have differential expression in normal and neoplastic
RT B cells.";
RL Am. J. Pathol. 163:135-144 (2003).
RC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; AY220118; AA05242.1; --
DR HSSP; P05154; 1L08.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000295; Prot_inh_Lserp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINII.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 435 AA; 48569 MW; 21AA8D4B4C4A5983 CRC64;

Alignment Scores:

Pred. No.: 6.44e-153 Length: 435
Score: 2186.00 Matches: 429
Percent Similarity: 98.85% Conservative: 1
Best Local Similarity: 98.62% Mismatches: 5

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	2202	90.1	435	4	US-09-912-628-5		Sequence 5, Appli
2	1056	43.2	419	4	US-09-949-016-11541		Sequence 11541, A
3	1046	42.8	415	4	US-09-919-039-390		Sequence 390, App
4	889	36.4	422	4	US-09-244-111-8		Sequence 8, Appli
5	872	35.7	423	4	US-09-976-594-19		Sequence 19, Appl
6	872	35.7	423	4	US-09-919-039-19		Sequence 19, Appl
7	847.5	34.7	414	4	US-09-949-016-8143		Sequence 8143, Ap
8	778.5	31.9	405	1	US-07-829-954-2		Sequence 2, Appli
9	778.5	31.9	405	1	US-07-994-423-2		Sequence 2, Appli
10	778.5	31.9	405	1	US-08-421-891-2		Sequence 2, Appli
11	778.5	31.9	416	4	US-09-949-016-7597		Sequence 7597, Ap
12	768	31.4	418	1	US-08-121-714-3		Sequence 3, Appli

1 ATGCAAGGA

1 ATGCAAGGACAGGGCAGGAGAAGAGGAACTGCAAGACATATTTTGTTCCTCAAAATGGCA 60

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: October 9, 2005, 15:16:48 ; Search time 121 Seconds
(without alignments)
8994.176 Million cell updates/sec
Title: US-09-993-180-1_COPY_68_1375
Perfect score: 2444
Sequence: 1 atcaaggacagggcaggag.....aaatcccaataaattcttag 1308

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 3708224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool.p/US0993180/runat_07102005_180818_18731/app.query.fasta_1.1479
-DB=Published Applications AA -QFMT=faetan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=ext -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODES=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0993180_0CGN_1_130_@runat_07102005_180818_18731
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2225	91.0	435	10	US-09-993-180-2 Sequence 2, Appli
2	2202	90.1	435	9	US-09-912-628-5 Sequence 5, Appli
3	2124	86.9	417	10	US-09-946-374-236 Sequence 236, App
4	2124	86.9	417	13	US-10-052-586-452 Sequence 452, App
5	2124	86.9	417	14	US-10-174-590-452 Sequence 452, App
6	2124	86.9	417	14	US-10-176-758-452 Sequence 452, App
7	2124	86.9	417	14	US-10-175-737-452 Sequence 452, App
8	2124	86.9	417	14	US-10-174-581-452 Sequence 452, App
9	2124	86.9	417	14	US-10-176-483-452 Sequence 452, App
10	2124	86.9	417	14	US-10-176-749-452 Sequence 452, App
11	2124	86.9	417	14	US-10-176-914-452 Sequence 452, App
12	2124	86.9	417	14	US-10-176-915-452 Sequence 452, App
13	2124	86.9	417	14	US-10-173-706-452 Sequence 452, App
14	2124	86.9	417	14	US-10-175-738-452 Sequence 452, App
15	2124	86.9	417	14	US-10-175-752-452 Sequence 452, App
16	2124	86.9	417	14	US-10-176-482-452 Sequence 452, App
17	2124	86.9	417	14	US-10-176-757-452 Sequence 452, App
18	2124	86.9	417	14	US-10-176-913-452 Sequence 452, App
19	2124	86.9	417	14	US-10-180-552-452 Sequence 452, App
20	2124	86.9	417	14	US-10-180-557-452 Sequence 452, App
21	2124	86.9	417	14	US-10-173-700-452 Sequence 452, App
22	2124	86.9	417	14	US-10-174-572-452 Sequence 452, App
23	2124	86.9	417	14	US-10-174-579-452 Sequence 452, App
24	2124	86.9	417	14	US-10-174-582-452 Sequence 452, App
25	2124	86.9	417	14	US-10-174-588-452 Sequence 452, App
26	2124	86.9	417	14	US-10-175-739-452 Sequence 452, App
27	2124	86.9	417	14	US-10-175-740-452 Sequence 452, App
28	2124	86.9	417	14	US-10-175-743-452 Sequence 452, App
29	2124	86.9	417	14	US-10-176-488-452 Sequence 452, App
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31	2124	86.9	417	14	US-10-176-747-452 Sequence 452, App
32	2124	86.9	417	14	US-10-176-750-452 Sequence 452, App
33	2124	86.9	417	14	US-10-176-985-452 Sequence 452, App
34	2124	86.9	417	14	US-10-176-987-452 Sequence 452, App
35	2124	86.9	417	14	US-10-176-992-452 Sequence 452, App
36	2124	86.9	417	14	US-10-176-993-452 Sequence 452, App
37	2124	86.9	417	14	US-10-184-658-452 Sequence 452, App
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43	2124	86.9	417	14	US-10-174-585-452 Sequence 452, App
44	2124	86.9	417	14	US-10-174-586-452 Sequence 452, App
45	2124	86.9	417	14	US-10-175-747-452 Sequence 452, App

ALIGNMENTS

RESULT 1
US-09-993-180-2
; Sequence 2, Application US/0993180
; Publication No. US20030054445A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM LYMPH
; TITLE OF INVENTION: CELLS; LSI-01
; FILE REFERENCE: D0051.NP
; CURRENT APPLICATION NUMBER: US/09/993,180
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/248,434
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/257,610
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/282,745
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2